GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 24, 2002, 03:00:16 ; Search time 2290.66 Seconds
(without alignments)
6417.463 Million cell updates/sec

Title: US-09-525-998A-1
Perfect score: 1368
Sequence: 1 atgggcctctccaccgtgcc.....cgcccagtcttctcagatga 1368

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351947 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_htc:*
10: qb_est1:*
11: qb_est2:*
12: qb_htc:*
13: qb_qss:*
14: em_qss_fun:*
15: em_qss_hum:*
16: em_qss_inv:*
17: em_qss_pln:*
18: em_qss_pro:*
19: em_qss_rod:*
20: em_qss_vrt:*
21: em_qss_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	764.6	55.9	957	10	AL559050	AL559050 AL559050
2	689	50.4	889	10	AU117362	AU117362 AU117362
3	682.4	49.9	761	10	AU131978	AU131978 AU131978
4	680	49.7	942	10	AL529836	AL529836 AL529836
5	678.2	49.6	975	10	AL577008	AL577008 AL577008
6	668.6	48.9	974	11	BG180101	BG180101 602329676
7	667	48.8	718	11	BG680679	BG680679 602626965
8	638.4	46.7	837	10	AL522989	AL522989 AL522989
9	630.4	46.1	769	10	AL522226	AL522226 AL522226
10	625	45.7	636	11	BG035257	BG035257 602324771
11	605.2	44.2	969	11	BE871809	BE871809 601448388
12	601.4	44.0	643	11	BG680356	BG680356 602629252
13	588	43.0	811	11	BE342444	BE342444 602013123
14	564	41.2	845	10	AU125021	AU125021 AU125021
15	559	40.9	859	10	AU124446	AU124446 AU124446
16	559	40.9	936	11	BG681438	BG681438 602628106
17	556.6	40.7	767	10	AU142156	AU142156 AU142156
18	541.4	39.6	702	11	BE344496	BE344496 602014902
19	541	39.5	971	11	BE876920	BE876920 601488490
20	540.6	39.5	772	10	AU137990	AU137990 AU137990
21	525.8	38.5	817	10	AU125680	AU125680 AU125680
22	513.8	37.5	761	11	BG282718	BG282718 602406578
23	508	37.1	524	11	BF720477	BF720477 mab54g09.y
24	506.4	37.0	786	10	AU124156	AU124156 AU124156
25	496.8	36.3	929	11	BG677121	BG677121 602623792
26	490.2	35.8	802	10	AU142163	AU142163 AU142163
27	489.8	35.8	805	10	AU125694	AU125694 AU125694
28	489	35.7	712	10	BE549214	BE549214 601078765
29	488.8	35.7	834	10	AU126303	AU126303 AU126303
30	486.8	35.6	788	10	AU124519	AU124519 AU124519
31	473	34.6	942	11	BE869492	BE869492 601446157
c 32	462.8	33.8	491	11	BF839822	BF839822 RC2-HT1023
33	461.4	33.7	822	11	BI607829	BI607829 602371033
34	454.8	33.2	779	10	AI119338	AI119338 qt04d04.y
c 35	452.8	33.1	960	10	AL529835	AL529835 AL529835
36	449	32.8	475	10	BF710028	BF710028 IL3-HT1061
37	437.6	32.0	742	10	AU125646	AU125646 AU125646
38	430.4	31.5	934	11	BG257964	BG257964 602379540
c 39	428.4	31.3	1095	11	BG745918	BG745918 602724961
40	415.6	30.4	640	11	BG698499	BG698499 602659011
41	413	30.2	725	11	BG863025	BG863025 602796549
42	410.4	30.0	624	10	BE295225	BE295225 601175209
43	405.8	29.7	484	11	BF807089	BF807089 IL5-C1014
44	388	28.4	426	10	AW950103	AW950103 EST362068
45	387.6	28.3	612	10	AU139183	AU139183 AU139183

ALIGNMENTS

RESULT 1
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LOCUS AL559050 957 bp mRNA EST 16-FEB-2001
DEFINITION AL559[illegible] LLI_NPI006_T2 Homo sapiens cDNA clone [illegible] 5 prime, mRNA sequence.
ACCESSION AL559050
VERSION AL559050.1 GI:12994166
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 957)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
FEATURES Location/Qualifiers
source 1..957
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DJ010YB05"
/clone_lib="LLI_NPI006_T2"
/sex="male"
/tissue_type="T cells from T cell leukemia"
/note="Vector: pCMVSPORT 6; Site_1: Not1; 1st strand cDNA was primed with a Not I,(dT)30 primer. Five prime end enriched, double stranded cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Femlialor Life Technologies, a division of Invitrogen 9900 Medical Center Drive

```
                    Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                    Email : lliang@elitetech.com URL :
                    http://fulllength.invitrogen.com"
BASE COUNT      222 a    262 c    252 g    220 t      1 others
ORIGIN


  Query Match             55.9%;  Score 764.6;  DB 10;  Length 957;
  Best Local Similarity   99.9%;  Pred. No. 3.5e-162;
  Matches  764;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 atgggcctctccaccgtgcctgacctgctgctgccactgctgctcctgcaagctgttgctg 60
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Db     193 ATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGCTGCTCCTGCAGCTGTTGCTG 252

Qy      61 ggaatatacccctcagggattattggactggtcctcacctagggacagggagaagaga 120
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Db     253 GGAATATACCCCTCAGGGATTATTGGACTGGTCCTCACCTAGGGACAGGGAGAAGAGA 312

Qy     121 gataagtgtgtgtccccaaggaaaatatatccacccctcaaaataattccgatttgctgtacc 180
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Db     313 GATAGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 372

Qy     181 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccgggggcaggatacggac 240
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Db     373 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 432

Qy     241 tgcagggagtgtgagagcgggctccttcaccgcttcagaaaaccacctcagacagtgcctc 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     433 TGCAGGGAGTGTGAGAGCGGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACAGTGCCTC 492

Qy     301 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     361 cgggacaccgtgtgtggctgcaggaaggaaccagtaccgggcattattggagtgaaaacctt 420
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Db     553 CGGGACACCGTGTGTGGCTGCAGGAAGGAACCAGTACCGGGCATTATTGGAGTGAAAACCTT 612

Qy     421 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcaccctctcctgccaggaag 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     613 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCCTCTCCTGCCAGGAG 672

Qy     481 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagaggaaaacgagtgtgtc 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     673 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAACAGAAAACGAGTGTGTC 732

Qy     541 tcctgtaagtaactgtaaggaaaggcctgaagtgcacgaaagttgtgcctaccccagattgag 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     733 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 792

Qy     601 aatgttaagggcactgagactcagccaccacagtgctgttgccccctggtcattttcttt 660
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Db     793 AATGTTAAGGGCACTGAGGACTCAGCCACCACAGTGCTGTTGCCCCTGGTCATTTTCTTT 852

Qy     661 ggtctttgccttttatcccctcctcttcattggttaatgtatcgctaccaacgctgcaaag 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     853 GGTCTTTGCCTTTTATCCCCTCCTCTTCATTGGTTTAATGTATCGCTACCAACGCTGCAAG 912

Qy     721 tccaagctctactccattgtttgtgggaaatcgaccacctgaaaaa 765
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Db     913 TCCAAGCTCTACTCCATTGTTTGTGGGAAATCGACACCTGAAAAA 957


RESULT   2
AU117362
LOCUS       AU117362      889 bp    mRNA            EST       19-OCT-2000
DEFINITION  AU117362 HEMBA1 Homo sapiens cDNA clone HEMBA1001229 5', mRNA
            sequence.
ACCESSION   AU117362
VERSION     AU117362.1  GI:10932324
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 889)
  AUTHORS   Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
            Yamamoto,J., Wakamatsu,A., Nakamura,Y., Naqai,T., Sugano,S. and
            Isogai,T.
  TITLE     HRI human cDNA project
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292 0812, Japan
            Tel. 81-438-52-3951
            Fax: 81-438-52-3952
            Email. genomics@hri.co.jp
            HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
            Research Institute, cDNA library construction: Department of
            Virology, Institute of Medical Science, University of Tokyo, and
            Helix Research Institute.
FEATURES             Location/Qualifiers
     source          1. .889
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                     /clone_lib="HEMBA1"
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                     /note="Vector: pME18SFL3"
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ORIGIN


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  Best Local Similarity   99.4%;  Pred. No. 3.8e-145;
  Matches  708;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy     665 tttgccttttatcccctcctcttcattggtttaatgtatcgctaccaacgctgcaaagtcca 724
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TTTGCCTTTTATCCCCTCCTCTTCATTGGTTTAATGTATCGCTACCAACGCTGCAAGTCCA 60

Qy     725 agctctactccattgtttgtgggaaatcgaccacctgaaaaaagaggggagcttgaaggaa 784
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AGCTCTACTCCATTGTTTGTGGGAAATCGACACCTGAAAAAGAGGGGGAGCTTGAAGGAA 120

Qy     785 ctactactaagccccctggcccccaaaccccaagcttcagtcccactccaggcttcaccccca 844
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Db     121 CTACTACTAAGCCCCTGGCCCCCAAACCCCAAGCTTCAGTCCCACTCCAGGCTTCACCCCCA 180

Qy     845 ccctqqqcttcagtcccqtqcccaqttccacctcacctcccaqctccacctataccccccq 904
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Qy     905 gtgactgtcccaacttgcqgctccccqcaqaqaqgtqqcaccacctatcaqqqqqctq 964
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Db     241 GTGACTGTCCCAACTTGCGGCTCCCCGCAGAGAGGTGGCACCACCCTATCAGGGGGCTG 300

Qy     965 acccctcttgcgacaqcccctqcctccqaccccatcccccaaccccctcaqaaqtqqq 1024
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Qy    1025 aqqacaqcqcccacaaqccacaqaqcctaqacactqatqacccqcqcaqcqctqtacqccq 1084
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 AGGACAGCGCCCACAAGCCACAGAGCCTAGACACTGATGACCCCGCGCAGCGTGTACGCCG 420

Qy    1085 tqqtqqaqaacgtqccccqttqcqctqqaaqqaattcgtqcqqcgcctaqqqctqaqcq 1144
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Qy    1145 accacgagatcgatcggctggagctgcagaacgggcgctgcctgcgcgaggcgcaatacg 1204
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Qy   1265 gacgcgtgctccgcgacatggacctgctgggctgctctggaggacatcgaggaggcgctttt 1324
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Db    601 GACGCGTGCTCCGCGACATGGACCTGCTGGGCTGCTCTGGAGGACATCGAGGAGGCGCTTT 660

Qy   1325 gcggccccgcgccctccccgcgcccagtcttctcagatga 1368
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Db    661 GCGGNCCCGCCG-CCTCCCGNCCGNGCCCAGTCTTCTCAGATGA 703


RESULT   3
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LOCUS       AU131978      761 bp    mRNA            EST       24 OCT 2000
DEFINITION  AU131978 NT2RP3 Homo sapiens cDNA clone NT2RP3003570 5', mRNA
            sequence.
ACCESSION   AU131978
VERSION     AU131978.1  GI:10992332
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 761)
  AUTHORS   Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
            Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
            Isogai,T.
  TITLE     HRI human cDNA project
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3951
            Fax: 81-438-52-3952
            Email: genomics@hri.co.jp
            HRI human cDNA project: 5' & 3'-end one pass sequencing: Helix
            Research Institute; cDNA library construction: Department of
            Virology, Institute of Medical Science, University of Tokyo, and
            Helix Research Institute.
FEATURES             Location/Qualifiers
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                     /clone_lib="NT2RP3"
                     /cell_type="teratocarcinoma"
                     /cell_line="NT2"
                     /note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
                     cells after 2 weeks retinoic acid (RA) induction"
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ORIGIN


  Query Match             49.9%;  Score 682.4;  DB 10;  Length 761;
  Best Local Similarity   99.1%;  Pred. No. 1.1e-143;
  Matches  694;  Conservative    0;  Mismatches    5;  Indels    1;  Gaps    1;

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Db     62 ATGCCCCTCTCCACCGTGCCTGACTTGCTCTGCGCACTGGATGCCTCCTGGAGGTCTTGGTG 121

Qy     61 ggaatataccctcaggggttattggactggtccctcaactagggacaggagaagaga 120
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Db    122 GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCAACTAGGGACAGGAGAAGAGA 181

Qy    121 gatagtgtgtgtccccaaggaaaatatatccacccttaaaataattcgatttgctgtacc 180
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Qy    181 aagtgccacaaaaggaacctactttatacaatgaactgtccaagtccggggcaggatacggac 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    241 tgcaggaaatatgtgaagtgcagtctcttcaccgcttcaggaaaacaactcaaacatgcctc 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    302 TGCAGGGAGTATGTGAAGTGCGGCTCCTTCACCGCTTCAGAAAACAACTCA AGACATGCCTC 361

Qy    301 aactgtcccaaatgcccaaaagaaaatttcaaatttaaatatcttcttttgcacaatgcgac 360
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Db    362 AGCTGCCCCAAATGCCCAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 421

Qy    361 cdqqaacaccatgtatgactgcaqqaaaaacaatacccgcattattgcaatgaaaaccctt 420
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Db    422 CGGGACACCGTGTGTGGCTGTAGGAAGAACAGTACCGG ATTATTGGAATGAAAACCTT 481

Qy    421 ttccaatgcttcaattgcaggcctctgcctcaatgggacatgcacctctgccagggag 480
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Qy    481 aaaacaaaaaaaccatatacacctgcaatgaaggttttcttttaaaaaaaaaacgaagtgtgtc 540
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Db    542 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGACAAAACCAGTGTGTC 601

Qy    541 tcctgtatcaatgtgaaaaaaatctgaaatcaaaaaaaaaaaaaaaaaaaaaaaaaaaag 600
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Db    602 TNCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAATTGTGTGCTACCCAGATTGAG 661

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Qy    660 tggtctttgcctttatcccctatctttcattgattttaatg 699
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Db    722 TGGTCTTTGCCTTTTATGCCTNCTTTCATTGTTTTAATG 761


RESULT   4
AL529836
LOCUS       AL529836      942 bp    mRNA            EST       13 FEB 2001
DEFINITION  AL529836 LIT_NFL001_NBC4 Homo sapiens cDNA clone CS0DB002YP05 5
            prime, mRNA sequence.
ACCESSION   AL529836
VERSION     AL529836.1  GI:12793329
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 942)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1..942
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone "CS0DB002YP05"
                     /clone_lib="LIT_NFL001_NBC4"
                     /sex="male"
                     /tissue_type "neuroblastoma cells"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a Not I-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed
                     by Life Technologies. Contact : Feng Liang Life
                     Technologies, a division of Invitrogen, 9800 Medical Center
                     Dri ve, Rockville, Maryland, 20850, USA Fax : (1) 301 610
```

```
                    8371 Email : fliang@lifetech.com URL :
                    http://fulllength.invitrogen.com"
BASE COUNT      208 a    259 c    248 g    224 t      3 others
ORIGIN


  Query Match             49.7%;  Score 680;  DB 10;  Length 942;
  Best Local Similarity   99.0%;  Pred. No. 4.1e-143;
  Matches  703;  Conservative    2;  Mismatches    3;  Indels    2;  Gaps    2;

Qy       1 atgggcctctccaccgtgcctgacctgctgctgccactggtgctcctggagctgttggtg 60
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db     234 ATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGCTCCTGGAGCTGTTGGTG 293

Qy      61 ggaatataccccctcagggttattggactggtccctcacctaggggacaggggaggaagaga 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     294 GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGAGGAAGAGA 353

Qy     121 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     354 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 413

Qy     181 aagtgccacaaaggaacctacttgtacaatgactgtccaggccccgggcaggatacggac 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     414 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 473

Qy     241 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     474 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 533

Qy     301 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     534 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 593

Qy     361 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     594 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 653

Qy     421 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     654 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 713

Qy     481 aaacagaacaccgtgtgcacctgccatgcagg-tttctttctaagagaaaacgagtgtgt 539
           |||||||||||||||||||||||||||||||| |||||||||||||| ||||||||||||
Db     714 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTTCTTTCTAAGAGAAACGAGTGTGT 773

Qy     540 ctcctgtagtaactgtaaagaaaagcctgaagtgcacgaagttgtgcctacccagattga 599
           |||||||||||||||||||:|||||||||||||||| ||||||||||||||||||||||||
Db     774 CTCCTGTAGTAACTGTAAGAGAAGCCTGGAGTGCACG-AGTTGTGCCTACCCCAGATTGA 832

Qy     600 gaatgttaagggcactgaggactcaggcaccacagtgctgttgccccctggtcatttttctt 659
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     833 GAATGTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGTTGCCCCTGGTCATTTTCTT 892

Qy     660 tggtctttgccttttatccctcctcttcattggtttaatgtatcgctacc 709
           |||||| |||||||||:|||||||||||||||||||||||||||||||
Db     893 TGGTCTGTGCCTTTTATMCCTCCTCTTCATTGGTTTAATGTATCGCTACC 942


RESULT   5
AL577008
LOCUS       AL577008      975 bp    mRNA            EST       16-FEB-2001
DEFINITION  AL577008 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI082YA01 5
            prime, mRNA sequence.
ACCESSION   AL577008
VERSION     AL577008.1  GI:12939716
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 975)
  AUTHORS   Li,W.B., Gruber,C., Jossee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1..975
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone "CS0DI082YA01"
                     /clone_lib="LTI_NFL006_PL2"
                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      231 a    258 c    259 g    221 t      6 others
ORIGIN


  Query Match             49.6%;  Score 678.2;  DB 10;  Length 975;
  Best Local Similarity   97.9%;  Pred. No. 1.1e-142;
  Matches  704;  Conservative    4;  Mismatches    8;  Indels    3;  Gaps    2;

Qy       1 atgggcctctccaccgtgcctgacctgctgctgccactggtgctcctggagctgttggtg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     256 ATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGCTCCTGGAGCTGTTGGTG 315

Qy      61 ggaatataccccctcagggttattggactggtccctcacctaggggacaggggaggaagaga 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     316 GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGAGGAAGAGA 375

Qy     121 gatagtgtgtgtccccaaggaaaatatatccaccctcaaaataattcgatttgctgtacc 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     376 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 435

Qy     181 aagtgccacaaaggaacctacttgtacaatgactgtccaggccccgggcaggatacggac 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     436 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGAC 495

Qy     241 tgcagggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     496 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 555

Qy     301 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     556 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 615

Qy     361 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaacctt 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     616 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 675

Qy     421 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     676 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 735

Qy     481 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaaagaaaaacgagtgtgtc 540
           |||||||||||||||||| |||||||||||| ||||||||||||||||||||||||||||
Db     736 AAACAGAACACCGTGTGCCCCTGCCATGCAGTTTTCTTTCTAAGAGAAAACGAGTGTGTC 795

Qy     541 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttg-tgcctaccccagattga 599
           |:||||||||||||:|||||||||||||||||||||||||| ||||||||||||||||||
Db     796 TYCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGSTGCCTACCCCAGATTGA 855

Qy     600 gaatgttaagggcactgaggactcaggcaccacagtgctgttgccccctggtcatttttctt 659
           ||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db     856 GAATGTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGTTGCCCCTGGTCATTTTCTT 915
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Db    856 GAATGTTAAGGGCACTGAGGACTCAGGCACCAMAGTGCTGTTGCCCCTGGTCATTTTCTT 915

Qy    660 tgatctttgccttttatgcctcctcttgattgatttaatgtatcgctaccaaacgttgga 718
          ||||||||||||||||   || |||||||||||||||||||||||||||||||| | |
Db    916 TGGTGTTTGGCTTT--ATGCCCCTCTTCATTGGTTTAATGTATCGCTACCAASGTGGAA 972


RESULT   6
BG180101
LOCUS       BG180101      974 bp    mRNA            EST       06-FEB-2001
DEFINITION  602329676F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4431019 5',
            mRNA sequence.
ACCESSION   BG180101
VERSION     BG180101.1  GI:12686804
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 974)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10185  row: q  column: 20
            High quality sequence stop: 657.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4431019"
                     /clone_lib="NIH_MGC_91"
                     /tissue_type="adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.4 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      259 a    265 c    265 g    185 t
ORIGIN


  Query Match             48.9%;  Score 668.6;  DB 11;  Length 974;
  Best Local Similarity   95.3%;  Pred. No. 1.6e-140;
  Matches  689;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy      4 gacctctccaccgtgcctgacctactgctgtgccactggtgctcctggagctgttggtgtggga 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGCCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGCTCCTGGAGCTGTTGGTGTGGGA 60

Qy     64 atatacccctcaggggttattgqactggtcccctcacctagggacagggagaagagagat 123
          ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db     61 ATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGACAGGGAGAAGAGAGAT 120

Qy    124 agtgtgtgtccccaaqqaaaatatatccacccctcaaaatgattccgatttgctgtaccaag 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGTGTGTGTCCCCAAGCAAAATATATCCACCCTCAAAATGATTCCGATTTGCTGTACCAAG 180

Qy    184 tgccacaaaggaacctacttgtacaatgactgtccaggcccgggggcaggatacggactgc 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGACTGC 240

Qy    244 agqqagtgtgaqaqcqggctcvttcacgcttcagaaaacccctcagacactgcctcagc 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    241 AGGGAGTGTGAGAGCGGCTCGTTCACGCTTCAGAAAACCCCTCAGACACTGCCTCAGC 300

Qy    304 tgcttcaaatgcaaaaaaaaaatttcaaatcaatcaaatcttcttcaaqqtqqcacccqq 363
          |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGCTGCAAATGCGGAAAGGAAATCGGTCAGGTCGTCAGTCGTCTGCACAGTGGACCGG 360

Qy    364 gacacccgtgtgtqqctgcaggaaaaacctqatacqqccattattggaqtqaaaaacttttc 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GACACCGTGTGTGGCTGCAGGAAGAACCTGATACGGCCATTATTGGAGTGAAAAACTTTTC 420

Qy    424 catctttaaattgaaatctatcaatgaaattttcttttaaaaaaaaaaaaatatatatcc 483
          ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CACTCTTTCAATTGCAGCCTCTGCCTCAATTCGCAGCCTCGCAGCCTCTCCTGCCAGGAGAAA 480

Qy    484 cgaaaacaaaaatatgaactatgcaaatttcttt taaaaaaaaaaaaatatatatcc 543
          |||||||||:|||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db    481 CAGAACACGGTGTGCACCTGCCACAGCTTTCTTTTAAGAGAAAACGAGTGTGTCTCC 540

Qy    544 tgtagtaactgtaaaaaaaqcctqqaqtgcacrqaaqttqtqcctacrcccaqattqaqaat 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACTCCCAGATTGAGAAT 600

Qy    604 attaaqqqcactqaqqactcaqqcactcaqtactattqcctcctaatcatttttctttqqt 663
          |||||||||||:|||||||||||||||||||||||||||||-|||  |   |||  || |
Db    601 GTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGTTGCCCTGGTCATTTTCTTTGGTC 660

Qy    664 ctttqctttqtcctcctctttcattqttaatatatctatcaaaaactqqqqqatcc 723
          ||||||||||| |||||||||| ||| |||        | |||||||||||||||||||
Db    661 TTTTGCCTTTTATTGCTGCTCTTCAGTGGCGTAAATGTAGTTGCTGCTGCCACGCGGAAGCCC 720

Qy    724 aaq 726
          | |
Db    721 AGG 723


RESULT   7
BG680679
LOCUS       BG680679      718 bp    mRNA            EST       01-MAY-2001
DEFINITION  602626965F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4751536 5',
            mRNA sequence.
ACCESSION   BG680679
VERSION     BG680679.1  GI:13912076
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 718)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10608  row: b  column: 17
            High quality sequence stop: 679.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /clone_lib="NCI_CGAP_Skn4"
                     /tissue_type="squamous cell carcinoma"
                     /lab_host="DH10B (11 phage-resistant)"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: oligo dT.
                     Average insert size 1.5kb.  Library constructed by Life
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Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 134 a 254 c 198 g 132 t
ORIGIN

Query Match 48.8%; Score 667; DB 11; Length 718;
Best Local Similarity 98.4%; Pred. No. 3.4e-140;
Matches 684; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 654 tttctttggtctttgccttttatcccctcttcattggtttaatgtatcgctaccaacg 713
Db 1 TTTCTTTGGTCTTTGCCTTTTATCCCTCCTCTTCATTGGTTTAATGTATCGCTACCAACG 60

Qy 714 gtggaaagtccaaggctctactccattgtttgtgggaaaatcgacacctgaaaaaagaggggga 773
Db 61 GTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCGACACCTGAAAAACACGCCGA 120

Qy 774 gcttgaaggaactactactaagccccctggccccaaacccaagcttcagtcccactccagg 833
Db 121 GCTTGAAGGAACTACTACTAAGCCCCTGGCCCCAAACCCAAGCTTCAGTCCCACTCCAGG 180

Qy 834 cttcacccccacccctgggcttcagtcccgtgcccagttccacttcacctcagctgcac 893
Db 181 CTTCACCCCCACCCTGGGCTTCAGTCCCGTGCCCAGTTCCACCTTCACCTCCAGCTCCAC 240

Qy 894 ctataccccggtgactgtcccaactttgcggctcccccgcagagaggtggcaccaccctа 953
Db 241 CTATACCCCCGGTGACTGTCCCAACTTTGCGGCTCCCCCGCAGAGAGGTGGCACCACCCTA 300

Qy 954 tcaggggctgaccccatcttgcgacagccctcgcctccgacccccatcccccaatccccct 1013
Db 301 TCAGGGGCTGACCCCATCTTGCGACAGCCCTCGCCTCCGACCCCATCCCCCAATCCCCT 360

Qy 1014 tcagaagtgggaggacagcgcccacaagccacagagcctagacactgatgaccccgcgac 1073
Db 361 TCAGAAGTGGGAGGACAGCGCCCACAAGCCACAGAGCCTAGACACTGATGACCCCGCGAC 420

Qy 1074 gctgtacgccgtggtggaggaacgtgccccgttgcgctggaaggaattcgtgcggccgcct 1133
Db 421 GCTGTACGCCGTGGTGGAGGAACGTGCCCCGTTGCGCTGGAAGGAATTCGTGCGGCCGCCT 480

Qy 1134 agggctgagcgaccacgagatcgatcggctggagctgcagaacgggcgctgcctgcgcga 1193
Db 481 AGGGCTGAGCGACCACGAGATCGATCGGCTGGAGCTGCAGAACGGGCGCTGCCTGCGCGA 540

Qy 1194 ggcgcaatacagcatgctggcgacctggagggcggcgcacgccgcgggcgcgaggccacgct 1253
Db 541 GGCGCAATACAGCATGCTGGCGACCTGGAGGGCGGCGCACGCCGCGGGCGCGAGGCCACGCT 600

Qy 1254 ggagctgctgggacgcgtgctccgcgacatggacctgctgggctgcctggagg-acatcg 1312
Db 601 GGAGCTGCTGGGACGCGTGCTCCGCGACATGGACCTGCTGGGCTGCCTGGAGGCACATCG 660

Qy 1313 aggaggcgcttgcgggccccgccgccctccgccc 1347
Db 661 AGGAGGCGCTTGCGGGCCCCGCCGACCCTCCCGACC 695

RESULT 8
AL522989
LOCUS AL522989 837 bp mRNA EST 13-FEB-2001
DEFINITION AL522989 LTI_NFL004_NBC2 Homo sapiens cDNA clone CS0DB009YP14 5 prime, mRNA sequence.
ACCESSION AL522989
VERSION AL522989.1 GI:12796492
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
REFERENCE 1 (bases 1 to 837)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES Location/Qualifiers
source 1..837
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DB009YP14"
/clone_lib="LTI_NFL004_NBC2"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a Not I-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Mary and 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT 199 a 231 c 229 g 177 t 1 others
ORIGIN

Query Match 46.7%; Score 638.4; DB 10; Length 837;
Best Local Similarity 99.8%; Pred. No. 9.8e-134;
Matches 639; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 atgggcctctccaccgtgcctgacctgctgctgccactggtgctcctggaggctgttggtg 60
Db 198 ATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGCTCCTGGAGGCTGTTGGTG 257

Qy 61 ggaatatacccctcagggattattggactggtccctcacctagggacagggagaagaga 120
Db 258 GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGACAGGGAGAAGAGA 317

Qy 121 gatagtgtgtgtccccaaggaaaatatatccacccтcaaaataattcgatttgctgtacc 180
Db 318 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTGCTGTACC 377

Qy 181 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccgggcaggatacggac 240
Db 378 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGCCAGGATACGGAC 437

Qy 241 tgcagggagtgtgaagagcggctcctcaccgcttcagaaaaccacctcagacactgcctc 300
Db 438 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 497

Qy 301 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 360
Db 498 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 557

Qy 361 cgggacaccgtgtgtggctgcaggaagaaccagtaccggcattattggagtgaaaaccтt 420
Db 558 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT 617

Qy 421 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 480
Db 618 TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 677

Qy 481 aaacgaacaccgtgtgcacctgccatgcagtttctttctaagagaaaacgagtgtgtc 540
Db 678 AAACAGAACACCGTGTGCACCTGCCATGCAGTTTCTTTCTAAGAGAAAACGAGTGTGTC 737

Qy 541 tcctgtagtaactgtaagaaaagcctgaagtgcacgaagttgtgcctacccccagattgag 600
Db 738 TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCCAGATTGAG 797

Qy 601 aatgttaagggccattgaggactcaggcaccctcagtatgtgt 640

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Db        798 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGT 837

RESULT    9
AL522226
LOCUS       AL522226       769 bp    mRNA            EST       13 FEB 2001
DEFINITION  AL522226 LTI_NFL004_NHC2 Homo sapiens cDNA clone CS0DB007YD05 5
            prime, mRNA sequence.
ACCESSION   AL522226
VERSION     AL522226.1  GI:12785719
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 769)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1..769
                     /organism="Homo sapiens"
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                     /sex="male"
                     /tissue_type="neuroblastoma cells"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed
                     by Life Technologies. Contact : Feng Liang Life
                     Technologies, a division of Invitrogen 9800 Medical Center
                     Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
                     8371 Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      145 a    273 c    225 g    126 t
ORIGIN


  Query Match             49.1%;  Score 630.4;  DB 10;  Length 769;
  Best Local Similarity   99.5%;  Pred. No. 6.1e-132;
  Matches  643;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    1;

Qy        723 caagctctactccattgtttgtgggaaatcgacacctgaaaaagaggggagcttgaagg 782
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Db          1 CAAGCTCTACTCCATTGTTTGTGGGAAATCGACACCTGAAAAAGAGGGGAGCTTGAAGG 60

Qy        783 aactactactaagcccctggccccaaacccaagcttcagtcccactccaggcttcacccc 842
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AACTACTACTAAGCCCCTGGCCCCAAACCCAAGCTTCAGTCCCACTCCAGGCTTCACCCC 120

Qy        843 caccctgggcttcagtcccgtgcccagttccaccttcacctccagctccacctatacccc 902
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Db        121 CACCCTGGGCTTCAGTCCCGTGCCCAGTTCCACCTTCACCTCCAGCTCCACCTATACCCC 180

Qy        903 cggtgactgtcccaactttgcggctcccccgcagagaggtggcaccaccctatcaggggc 962
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Db        181 CGGTGACTGTCCCAACTTTGCGGCTCCCCCGCAGAGAGGTGGCACCACCCTATCAGGGGC 240

Qy        963 tgaccccatccttgcggacagccctcgcctccgacccccatccccaaccccttcagaagtg 1022
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGACCCCATCCTTGCGGACAGCCCTCGCCTCCGACCCCATCCCCAACCCCTTCAGAAGTG 300

Qy       1023 ggaggacagcgcccacaagccacagagcctagacactgatgacccggcgacgctgtacgc 1082
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Db        301 GGAGGACAGCGCCCACAAGCCACAGAGCCTAGACACTGATGACCCGGCGACGCTGTACGC 360

Qy       1083 cgtggtggaaaacgtgcccccgttgcgctggaaggaattcgtgcggagcgctagggctgag 1142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGTGGTGGAGAACGTGCCCCCGTTGCGCTGGAAGGAATTCGTGCGGAGCCTAGGGCTGAG 420

Qy       1143 [illegible] 1202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CGACCACGAGATCGATCGGCTGGAGCTGCAGAACGGGCGCTGCCTGGCGAGGCGCAATA 480

Qy       1203 [illegible] 1262
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Db        481 CAGCATGCTGCGACCTGGAGGCGCGCACGC--GGGCGGAGGCTACGCTGGAGCTGCT 538

Qy       1263 [illegible] 1322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 GGGACGCGTGCTGCGTGACATGGACCTGCTGGGCTGCCTGGAGGACATCGAGGAGGCGCT 598

Qy       1323 ttgcggccgcgccgccctcccgccgcgcccagtcttctagatga 1368
              ||||||||||||||||||||||||||||||||||||||||||||
Db        599 TTGCGGCCGCGCCGCCCTCCCGCCGCGCCCAGTCTTCTAGATGA 644


RESULT   10
BG035257
LOCUS       BG035257       636 bp    mRNA            EST       24 JAN 2001
DEFINITION  602324771F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4413112 5',
            mRNA sequence.
ACCESSION   BG035257
VERSION     BG035257.1  GI:12429209
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 636)
  AUTHORS   NIH MGC http://[illegible]
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: [illegible]
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10138  row: m  column: 17
            High quality sequence stop: 636.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_90"
                     /tissue_type="adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.7 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      118 a    234 c    183 g    101 t
ORIGIN


  Query Match             48.7%;  Score 625;  DB 11;  Length 636;
  Best Local Similarity   99.8%;  Pred. No. 9.8e-131;
  Matches  636;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy        727 ctctactccattgtttgtgggaaatcgacacctgaaaaagaggggagcttgaaggaact 786
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Db      1 CTCTACTCCATTCTTTGTGGCAAATCCACACCTGAAAAACAGGGGAGCTTGAAGGAACT 60

Qy    787 actactaagccccctqqccccaaaccaaqcttcaqtcccactccaqqcttcaccccacc 846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACTACTAAGCCCCTGGCCCCAAACCCAAGCTTCAGTCCCACTCCAGGCTTCACCCCCACC 120

Qy    847 ctqqqcttcaqtcccqtqcccaqttcccaccttcacctccaqctcccacctataccccccqqt 906
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Db    121 CTGGGCTTCAGTCCCGTGCCCAGTTCCACCTTCACCTCCAGCTCCACCTATACCCCCCGGT 180

Qy    907 qactatcccaacttttqcqqctcccccqcaqaqaqqtqqccaccacccctatcaqqqqqctqac 966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GACTGTCCCAACTTTGCGGCTCCCCCGCAGACAGGTGGCACCACCCTATCACCCCCCTCAC 240

Qy    967 cccatcctttqcqacaqcccctcqcctcccaccccatccccaaccccctttcaqaaqtqqqaq 1026
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Db    241 CCCATCCTTGCGACAGCCCTCGCCTCCGACCCCATCCCCAACCCCCTTCAGAAGTGGGAG 300

Qy   1027 gacagcqcccacaaqccacaqaqcctagacactqatgacccccqcqacqctgtacgcccqtg 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GACAGCGCCCACAAGCCACAGAGCCTAGACACTGATGACCCCGCGACGCTGTACGCCGTG 360

Qy   1087 qtqqaqaacqtqccccccqttqccqctqqaaqqaattcqtqccqqccqcctaqqqctqaqccqac 1146
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Db    361 GTGGCAACGTGCCCCCGTTGCCGCTGGAAGGAATTCGTGCCGGCGCCTACCGCTCAGCCAC 420

Qy   1147 cacqaqatcqatcqqctqqaqctqcaqqaccqqccqctacctqccqaaqqccacaatacaqc 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CACGAGATCGATCGGCTGGAGCTGCAGGACCGGCCGCTGCCTGCCGAGGCGCAATACAGC 480

Qy   1207 atqctqqcqacctqqaqqcqqcqcacqccqcqccqcqaqqccacqctqqaqctqctqqqa 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ATGCTGGCGACCTGGAGGCGGCGCACGCCGCGGCGCGAGGCCACGCTGGAGCTGCTGGGA 540

Qy   1267 cqcqtqctccqcqacatqqacctqctqqqctqcctqqaaqqacatcqaqqaqqcqcttqc 1326
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Db    541 CGCGTGCTCCGCGACATGGACCTGCTGGGCTGCCTGGAGGACATCGAGGAGGCGCTTTGC 600

Qy   1327 qqccccqccqcccctcccqcccqcqcccaqtcttctca 1363
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Db    601 GGCCCCGCCGCCCTCCCGCCCG-GCCCAGTCTTCTCA 636


RESULT  11
BE871809
LOCUS       BE871809      969 bp    mRNA            EST       20-OCT-2000
DEFINITION  601448388F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852525 5',
            mRNA sequence.
ACCESSION   BE871809
VERSION     BE871809.1  GI:10320585
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 969)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9574  row: o  column: 22
            High quality sequence stop: 642.
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                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.  Library constructed by Life
                     Technologies. "
BASE COUNT      281 a    273 c    241 g    174 t
ORIGIN


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  Best Local Similarity   95.4%;  Pred. No. 3.1e-126;
  Matches  700;  Conservative    0;  Mismatches   23;  Indels   11;  Gaps    7;

Qy    141 aaaatatatccac cctcaaaataattcgatttgctgtaccaagtgccacaaaggaacct 199
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Db      1 AAAATATATCCGCGCCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCT 60

Qy    200 actgtacaatgactgtccaggcccqqqqcaqgatacggactgcaqggaqtgtgaggccg 259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGACTGCAGCCACTGTCACAGCC 120

Qy    260 gctccttcaccgcttcagaaaaccacctcagacactgcctcagctgctccaaatgccgaa 319
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Db    121 GCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAA 180

Qy    320 aggaaatgggtcaggtggagatctcttcttgcacagtggaccgggacaccgtgtgtggct 379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCT 240

Qy    380 gcaggaagaaccagtaccggcattattggagtgaaaaccttttccagtgcttcaattgca 439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCA 300

Qy    440 gcctctgcctcaatgggaccgtgcacctctcctgccaggagaaacagaacaccgtgtgca 499
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Db    301 GCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCA 360

Qy    500 cctgccatgcaggtttcttctaagagaaaacgagtgtgtctcctgtagtaactgtaaga 559
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Db    361 CCTGCCATGCAGGTTTCTTTCTAAGACAAAACGAGTGTGTCTCCTGTAGTAACTGTAAGA 420

Qy    560 aaaqcctqqaqtqcacqaaqttqtqcctaccccaqattqaqaaatqttaaqqqcactqaqg 619
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Db    421 AAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAGAATGTTAAGGGCACTGAGG 480

Qy    620 actcaggcaccacagtgctgttg ccctggtcatttttcttggtctttgccttttatcc 678
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Db    481 ACTCAGGCACCACAGTGCTGTTGCCCCCTGGTCATTTTCTTCGGTCTTTGCCTTTTATCC 540

Qy    679 ctcctcttcattggtttaatgtatcgctaccaacggtggaagtccaaqctctactccatt 738
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Db    541 CTCCTCTTCATTGGTTAAATGTATCGCTACCAACGGTGGAAGTCC-AGCTCTACTCCATT 599

Qy    739 gttgtggqqqaatcqaqcacctqaaaaaqaqttqqaqctqaaqaaa.tactactaaqa.c 798
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Db    600 G TTGTGGCAAATCGACCCCTGACAAAGA-GGGGAGCTTGAAGGAACTACTACTAAGCCC 657

Qy    799 ctqqccccaaaccaaqcttcaqtcccactccaqqcttcaccccccacccctgqqcttcaqt 858
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Db    658 GTGGCCCAAAACCAAGTC----AAGCCACTCCAGGTTCACCCCACACCCGGGG-TCAGC 711

Qy    859 cccgtqcccaqttc 872
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Db    712 ACCGCGCCCAGTCC 725


RESULT  12
BG680356
LOCUS       BG680356      643 bp    mRNA            EST       01-MAY-2001
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DEFINITION  602629252F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4753981 5',
            mRNA sequence.
ACCESSION   BG680356
VERSION     BG680356.1  GI:13911253
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 643)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10614  row: h  column: 14
            High quality sequence stop: 630.
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                     /clone_lib="NCI_CGAP_Skn4"
                     /tissue_type="Squamous cell carcinoma"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; Primer: Oligo dT;
                     Average insert size 1.5kb; Library constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      135 a    219 c    185 g    104 t
ORIGIN
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  Query Match             44.0%;  Score 601.4;  DB 11;  Length 643;
  Best Local Similarity   98.0%;  Pred. No. 2.1e-125;
  Matches  630;  Conservative    0;  Mismatches   11;  Indels    2;  Gaps    2;

Qy     692 gtttaatgtatcgctaccaacggtggaagtccaagctctactccattgtttgtgggaaat 751
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Db       1 GTTTAATGTATCGCTACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAAT 60

Qy     752 cgatacctaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 811
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CGACACCTGAAAAAGAGGGGGAGCTTGAAGGAACTACTACTAAGCCCCTCGCCCCAAACC 120

Qy     812 caagcttcagtcccactccaggcttcaccccaccctgggcttcagtcccgtgcccagtt 871
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CAAGCTTCAGTCCCACTCCAGGCTTCACCCCCACCCTGGGCTTCAGTCCCGTGCCCAGTT 180

Qy     872 ccacctcaccctccagctccaccctataccccccggtgactgtcccaactttgcggctcccc 931
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Db     181 CCACCTTCACCTCCAGCTCCACCTATACCCCCCGTGACTGTCCCAACTTTGCGGCTCCCC 240

Qy     932 gcaggaggctgggcaccaccctatcagggggctgacccccatcctttgccgacagccctcgcct 991
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Db     241 GCAGAGAGGTGGGCACCACCCTATCAGGGGGCTGACCCCATCCTTTGCGACAGCCCTCGCCT 300

Qy     992 ccgaccccatccccaaccccttcaggagtgggaggacagcgccccacaagccaacagagcc 1051
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Db     301 CCGACCCCATCCCCAACCCCCTTCAGAAGTGGGAGGACAGCGCCCCACAAGCCAACAGAGCC 360

Qy    1052 tagacactgatgacccccgcagcgtgtacgccgtgctggagaacgtgccccctttgcgct 1111
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Qy    1172 aggacggcgacttcctcgccctgtcagtgaggcgcagtacgtcatgccgccgtcgcagcat 1230
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Db     481 AGAACGGGCGCTGCCTGCGCGAGGCGCAATACAGCATCTGGCAGAACTGGAGGCGGCGC 540

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Db     541 ACGCCGACGGAGCGAGCCGCCACGCTGGAGCCTGCTGGGACGCGTGCTCGCGACATGGACCT 600

Qy    1291 gctgggcatactggaggacatcgaggaggcgctatagcggacc 1332
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Db     601 GCTGGGCATACTGGAGGACATCGAGGAGGCGCTATAGCGGACC 643


RESULT  13
BF342334
LOCUS       BF342334      811 bp    mRNA            EST       22-NOV-2000
DEFINITION  602761223F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4148932
            5', mRNA sequence.
ACCESSION   BF342334
VERSION     BF342334.1  GI:11289317
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 811)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9409  row: n  column: 05
            High quality sequence stop: 714.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; Primer: Oligo dT;
                     Average insert size 1.57 kb; Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      150 a    284 c    245 g    132 t
ORIGIN
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Qy     745 qggaaatcgacacctgaaaaagagggggagcttgaagaactactactaagcccctggcc 804
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13 GGGAAATCGACACCTGAAAAAGAGGGGGAGCTTGAAGAACTACTACTAAGCCCCTGGCC 72

Qy     805 ccaaaccccaagcttcagtcccactccaggcttcaccccaccctgggcttcagtcccgtgc 864
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73 CCAAACCCCAAGCTTCAGTCCCACTCCAGGCTTCACCCCCACCCTGGGCTTCAGTCCCGTG 132

Qy     865 ccagttccacctccagctccaccctataccccccggtgactgtcccaactttgcggctccc 924
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Db     133 CCCAGTTCCACCTTCACCTCCAGCTCCACCTATACCCCCGGTGACTGTCCCAACCTTGCG 192

Qy     925 gctccccgcagaagagtggtgaaccaccctatcaggggctgaccccatccttgcgacagcc 984
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     193 GCTCCCCGCAGACAGCTGCCACCACCCTATCAGGGGCTGACCCCATCCTTGCGACAGCC 252

Qy     985 ctcgcctccgaccccatccccaaccccctlcaqaaqtqqqaqgacaqcgcccacaaqcca 1044
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     253 CTCCCCTCCCACCCCATCCCCAACCCCCTTCAGAAGTGGCAGGACAGCGCCCACAAGCCA 312

Qy    1045 cagaqcctagacactgatgacccccgcgacgctgtacgccgtggtggagaaccgtgcccccg 1104
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     313 CAGAGCCTAGACACTGATGACCCCCGCACGCTGTACGCCGTGGTGGAGAACCGTGCCCCCG 372

Qy    1105 ttgcgctggaaqgaattcgtgcgccgccctaqggctgagcgaccaccagatcgatccgctg 1164
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     373 TTGCGCTGGAAGCAATTCGTGCCGCCGCCTAGGCTGAGCGACCACCAGATCGATCCGCTG 432

Qy    1165 qagctgcagaacgggcgctgcctgcgcgaagcgcaatacagcatgctggcgacctgqaagg 1224
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
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Qy    1225 cggcgcacgccgcggcgcgaggccacgctggagctgctqqyacgcgtgctcvgcgacatg 1284
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     492 CGGCGCACGCCGCGGCGCGAGGCCACGCTGGAGCTGCTGGGACGCGTGCTCCGCGACATG 551

Qy    1285 gacctgctgggctgcctggaggacatcgagqaggcgctttqcggccccgccgccctcccg 1344
           ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db     552 GACCTGCTGGGCTGCCTGGAGGACATCGAGGAGGCGCTTTGCGG-CCCGCCGCCCTCCCG 610

Qy    1345 cccgcgcccaqtcttctcaqatga 1368
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Db     611 CCCG-GCCCAGTCTTCTCAGATGA 633


RESULT  14
AU125021
LOCUS       AU125021      845 bp    mRNA            EST       23-OCT-2000
DEFINITION  AU125021 NT2RM4 Homo sapiens cDNA clone NT2RM4000896 5', mRNA
            sequence.
ACCESSION   AU125021
VERSION     AU125021.1  GI:10949737
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 845)
  AUTHORS   Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J.,
            Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
            Isogai,T.
  TITLE     HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S.,
            Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki
            ,Y., Sugano,S., Isogai,T.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3951
            Fax: 81-438-52-3952
            Email: genomics@hri.co.jp
            HRI human cDNA project, 5'- & 3' end one pass sequencing. Helix
            Research Institute; cDNA library construction: Department of
            Virology, Institute of Medical Science, University of Tokyo, and
            Helix Research Institute.
FEATURES             Location/Qualifiers
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                     /cell_line="NT2"
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ORIGIN


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Db     220 ATGGGCCTCTCCACCGTGCCTGACCGCTGCTGTGCCACTGATGCTCCTGGAGCTGTTGATG 279

Qy      61 ggaatatacccctcagggttattggactggtcccctcacctaggggacaggqaagaagaga 120
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Db     280 GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGGCAGGGAGAAGAGA 339

Qy     121 gataqtgtgtgtccccaaggaaaatatatccaccctcaaaatgattcgatttgctgtacc 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     340 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATGATTCGATTTGCTGTACC 399

Qy     181 aagtgccacaaaggaacctacttgtacaatgactgtccaggccggggcaggatacggac 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     400 AAGTGCCACAAAGGAACCTACTGTACAATGACTGTCCAGGCCGGGGCAGGATACGGAC 459

Qy     241 tgcaggagtgtgagagcggctccttcaccgcttcagaaaaccacctcagacactgcctc 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     460 TGCAGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 519

Qy     301 agctgctccaaatgccgaaaggaaatgggtcaggtggagatctcttcttgcacagtggac 360
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Db     520 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 579

Qy     361 cgggacaccgtgtgtggctgcaggaaggaaccaqtaccggcattattggagtgaaaacctt 420
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Qy     421 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcaccctctcctgccaggag 480
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Qy     481 aaacagaacaccgtgtgcacctgccatgcagqtttctttctaaqaqaaaacgagtgtgtc 540
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Db     700 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGA-TGTGTC 758

Qy     541 tcctgtagtaactgtaaqaaaaqcctgaagtgcacgaagttgtgcctaccccagattgag 600
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Db     759 TNCTGTAGTAACTGTAAGAAAAGCCT-GAATGCACGAAGTTGTGCCTACCC--ANATTG 814

Qy     601 aatgttaagggcactgaggactcaggcacca 631
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Db     815 AAATGTTAAGGCACTGAGGACTAGCNCCACA 845


RESULT  15
AU124446
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DEFINITION  AU124446 NT2RM4 Homo sapiens cDNA clone NT2RM4000818 5', mRNA
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ACCESSION   AU124446
VERSION     AU124446.1  GI:10949162
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 859)
  AUTHORS   Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J.,
            Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
            Isogai,T.
  TITLE     HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S.,
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            Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki
            ,Y., Sugano,S., Isogai,T.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3951
            Fax: 81-438-52-3952
            Email: genomics@hri.co.jp
            HRI human cDNA project; 5' & 3' end one pass sequencing: Helix
            Research Institute; cDNA library construction: Department of
            Virology, Institute of Medical Science, University of Tokyo, and
            Helix Research Institute.
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ORIGIN
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Matches 573; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

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Db     279 ATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGCTCCTGGAGCTGTTGGTG 338

Qy      61 qgaatatacccctcaggggttattggactggtcctcacctaggggacaggagaagaga 120
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Db     339 GGAATATACCCCTCAGGGGTTATTGGACTGGTCCTCACCTAGGGGACAGGAGAAGAGA 398

Qy     121 gatagtgtgtgtcccaaggaaaatatatccacctcaaaataattcgatttgctgtacc 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     399 GATAGTGTGTGTCCCAAGGAAAATATATCCACCTCAAAATAATTCGATTTGCTGTACC 458

Qy     181 aagtgccacaaaggaacctacttgtacaatgactgtccaggcccgggcaggatacggac 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     459 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGCCAGGATACGGAC 518

Qy     241 tgcaggaagtgtgaggagcggctcttcaccgcttcagaaaaccacctcagacactgcctc 300
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Db     519 TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 578

Qy     301 agctgctccaaatgccgaaaggaaatgggtcaggtggagatcttcttcttgcacagtggac 360
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Db     579 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTTCTTCTTGCACAGTGGAC 638

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Qy     421 ttccagtgcttcaattgcaggcttgcctcaatgggaccgtgcacctcttcctgccaggag 480
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Qy     481 aaacagaacaccgtgtgcacctgccatgcaggtttctttctaagagaaaacgagtgtgtc 540
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Qy     541 tcctgtagtaactgtaagaaaagcctggagtgcacgaagttg 582
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